

10/505315

60163PCT SEQ listing
SEQUENCE LISTING

DT09 Rec'd PCT/PTO 19 AUG 2004

<110> Syngenta Participations AG
Shen, Zhicheng
Warren, Gregory
Shotkoski, Frank
Kramer, Vance

<120> Novel vip3 Toxins and Methods of Use

<130> 60163PCT

<150> US 60/362250
<151> 2002-03-06

<160> 33

<170> PatentIn version 3.2

<210> 1
<211> 2367
<212> DNA
<213> Bacillus thuringiensis

<220>
<221> misc_feature
<222> (1)..(2367)
<223> Native vip3C coding sequence.

An "r" at position 2213 represents the nucleotide g or a.

<400> 1

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gatacaggtg gtaatctaac cttagacgaa atcctaaaga atcagcagtt actaa	180
atttctggta aattggatgg ggtaaattggg agcttaaattg atcttatcgc acag	240
gaaatacag aattatctaa ggaaattctta aaaatcgcaa atgaacagaa tcaag	300
aatgatgtta ataacaaact cgatgcgata aatacgatgc ttcatatata tctac	360
attacatcta tgtaagtga tgtaatgaag caaaattatg cgctaagtct gcaaata	420
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tcgcctgctg atattcttga tgagttaact gaattaactg aactagcgaa aagtgt	660
aaaaatgacg ttgatggttt tgaattttac cttatacat tccacgatgt aatgg	720
aataatttat tcgggcgttc agcttttaaaa actgcttcag aattaattgc taaag	780
gtgaaaacaa gtggcagtgag agtaggaaat gtttataatt tcttaattgt attaa	840
ctacaagcaa aagcttttct tactttaaca acatgccgaa aattattagg cttag	900

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attgattata cttctattat gaatgaacat ttaaataagg aaaaagagga atttagagta 960
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agtgatgaag atgcaaagat gattgtggaa gctaaaccag gacatgcatt ggttgggttt 1080
gaaatgagca atgattcaat cacagtatta aaagtatatg aggctaagct aaaacaaaat 1140
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aaatttacaa ttttagaaat taagcctgag gaggatttat taagcccaga attaattaat 2040
ccgaattcct ggattacgac tccaggggct agcatttcag gaaataaact tttcattaac 2100
ttggggacaa atgggacctt tagacaaagt ctttcattaa acagttattc aacttatagt 2160
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<210> 2
 <211> 788
 <212> PRT
 <213> *Bacillus thuringiensis*

<220>
 <221> MISC_FEATURE
 <222> (1)..(788)
 <223> Vip3C Toxin

The Xaa at position 738 is either the amino acid Glu or Gly.

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Ile Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile Lys Asp
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35 40 45

Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Glu Ile Ser Gly Lys
50 55 60

Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly Asn
65 70 75 80

Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn Glu Gln
85 90 95

Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu Asp Ala Ile Asn Thr
100 105 110

Met Leu His Ile Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser Asp Val
115 120 125

Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Ile Glu Tyr Leu Ser Lys
130 135 140

Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile Ile Asn Val Asn Val
145 150 155 160

Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile
165 170 175

Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr Glu Thr
180 185 190

Thr Leu Lys Val Lys Lys Asp Ser Ser Pro Ala Asp Ile Leu Asp Glu
195 200 205

Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val
210 215 220

Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val Gly
225 230 235 240

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Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile
245 250 255

Ala Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr
260 265 270

Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Lys Ala Phe Leu Thr
275 280 285

Leu Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Gly Ile Asp Tyr Thr
290 295 300

Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg Val
305 310 315 320

Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala
325 330 335

Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu Ala Lys
340 345 350

Pro Gly His Ala Leu Val Gly Phe Glu Met Ser Asn Asp Ser Ile Thr
355 360 365

Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln Val Asp
370 375 380

Lys Asp Ser Leu Ser Glu Val Ile Tyr Gly Asp Thr Asp Lys Leu Phe
385 390 395 400

Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Asn Asn Ile Val Phe
405 410 415

Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys Met Lys
420 425 430

Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly
435 440 445

Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala Glu Tyr
450 455 460

Arg Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr Met Pro Leu Gly Val
465 470 475 480

Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu Gln Ala
485 490 495

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Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr Leu Arg
500 505 510

Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile
515 520 525

Val Pro Pro Ser Gly Phe Ile Ser Asn Ile Val Glu Asn Gly Ser Ile
530 535 540

Glu Glu Asp Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn Ala Tyr
545 550 555 560

Val Asp His Thr Gly Gly Val Asn Gly Thr Lys Ala Leu Tyr Val His
565 570 575

Lys Asp Gly Gly Phe Ser Gln Phe Ile Gly Asp Lys Leu Lys Pro Lys
580 585 590

Thr Glu Tyr Val Ile Gln Tyr Thr Val Lys Gly Lys Pro Ser Ile His
595 600 605

Leu Lys Asp Glu Asn Thr Gly Tyr Ile His Tyr Glu Asp Thr Asn Asn
610 615 620

Asn Leu Lys Asp Tyr Gln Thr Ile Thr Lys Arg Phe Thr Thr Gly Thr
625 630 635 640

Asp Leu Lys Gly Val Tyr Leu Ile Leu Lys Ser Gln Asn Gly Asp Glu
645 650 655

Ala Trp Gly Asp Lys Phe Thr Ile Leu Glu Ile Lys Pro Ala Glu Asp
660 665 670

Leu Leu Ser Pro Glu Leu Ile Asn Pro Asn Ser Trp Ile Thr Thr Pro
675 680 685

Gly Ala Ser Ile Ser Gly Asn Lys Leu Phe Ile Asn Leu Gly Thr Asn
690 695 700

Gly Thr Phe Arg Gln Ser Leu Ser Leu Asn Ser Tyr Ser Thr Tyr Ser
705 710 715 720

Ile Ser Phe Thr Ala Ser Gly Pro Phe Asn Val Thr Val Arg Asn Ser
725 730 735

Arg Xaa Val Leu Phe Glu Arg Ser Asn Leu Met Ser Ser Thr Ser His
740 745 750

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Ile Ser Gly Thr Phe Lys Thr Glu Ser Asn Asn Thr Gly Leu Tyr Val
755 760 765

Glu Leu Ser Arg Arg Ser Gly Gly Gly Gly His Ile Ser Phe Glu Asn
770 775 780

Val Ser Ile Lys
785

<210> 3
<211> 2367
<212> DNA
<213> Artificial Sequence

<220>
<223> Maize optimized vip3C coding sequence.

An "r" at positions 2213 and 2214 represents the nucleotide g or a.

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<400> 3
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gacaccggcg gcaacctcac cctcgacgag atcctcaaga accagcagct cctcaacgag      180
atcagcggca agctcgacgg cgtgaacggc tccctcaacg acctcatcgc ccagggcaac      240
ctcaacaccg agctgtccaa ggagatcctc aagatcgcca acgagcagaa ccaggtgctc      300
aacgacgtga acaacaagct cgacgccatc aacaccatgc tccacatcta cttcccgaag      360
atcacctcca tgctctccga cgtgatgaag cagaactacg cctctcctt ccagatcgag      420
taccttcca agcagctcca ggagatcagc gacaagctcg acatcatcaa cgtgaacgtg      480
ctcatcaact ccacctcac cgagatcacc cgggcctacc agcgcacaa gtacgtgaac      540
gagaagttcg aggagctgac cttcgccacc gagaccacc tcaaggtgaa gaaggactcc      600
tccccggccg acatcctcga cgagctgacc gagctgaccg agctggccaa gtccgtgacc      660
aagaacgacg tggacggctt cgagttctac ctcaacacct tccacgacgt gatggtgggc      720
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gtgaagacct ccggctccga ggtgggcaac gtgtacaact tcctcatcgt gtcaccgcc      840
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atcgactaca cctccatcat gaacgagcac ctcaacaagg agaaggagga gttccgcgtg      960
aacatcctcc cgaccctctc caacaccttc tccaaccgca actacgcaa ggtgaagggc     1020
tccgacgagg acgccaagat gatcgtggag gccaagccgg gccacgccct cgtgggcttc     1080
gagatgtcca acgactccat caccgtgctc aagggtgtac aggccaagct caagcagaac     1140
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ttcgagcgct ccaacctcat gtctccacc tcccacatct ccggcacctt caagaccgag	2280
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<210> 4
 <211> 2370
 <212> DNA
 <213> Bacillus thuringiensis

<220>
 <221> misc_feature
 <222> (1)..(2370)
 <223> vip3A(a) native coding sequence.

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gatacaggtg gtgatctaac cctagacgaa attttaaaga atcagcagtt actaaatgat	180
atttctggta aattggatgg ggtgaatgga agcttaaatg atcttatcgc acagggaaac	240

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aactttatta	ttttggaaat	tagtccttct	gaaaagttat	taagtccaga	attaattaat	2040
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<210> 5
 <211> 789
 <212> PRT
 <213> Bacillus thuringiensis

<220>
 <221> MISC_FEATURE
 <222> (1)..(789)
 <223> Vip3A toxin

<400> 5

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Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asp Leu Thr Leu
 35 40 45

Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Asp Ile Ser Gly Lys
 50 55 60

Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly Asn
 65 70 75 80

Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn Glu Gln
 85 90 95

Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu Asp Ala Ile Asn Thr
 100 105 110

Met Leu Arg Val Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser Asp Val
 115 120 125

Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Ile Glu Tyr Leu Ser Lys
 130 135 140

Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile Ile Asn Val Asn Val
 145 150 155 160

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Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile
165 170 175

Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr Glu Thr
180 185 190

Ser Ser Lys Val Lys Lys Asp Gly Ser Pro Ala Asp Ile Leu Asp Glu
195 200 205

Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val
210 215 220

Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val Gly
225 230 235 240

Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile
245 250 255

Thr Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr
260 265 270

Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Lys Ala Phe Leu Thr
275 280 285

Leu Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp Tyr Thr
290 295 300

Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg Val
305 310 315 320

Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala
325 330 335

Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu Ala Lys
340 345 350

Pro Gly His Ala Leu Ile Gly Phe Glu Ile Ser Asn Asp Ser Ile Thr
355 360 365

Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln Val Asp
370 375 380

Lys Asp Ser Leu Ser Glu Val Ile Tyr Gly Asp Met Asp Lys Leu Leu
385 390 395 400

Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Asn Asn Ile Val Phe
405 410 415

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Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys Met Lys
420 425 430

Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly
435 440 445

Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala Glu Tyr
450 455 460

Arg Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr Met Pro Leu Gly Val
465 470 475 480

Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu Gln Ala
485 490 495

Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr Leu Arg
500 505 510

Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile
515 520 525

Val Pro Pro Ser Gly Phe Ile Ser Asn Ile Val Glu Asn Gly Ser Ile
530 535 540

Glu Glu Asp Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn Ala Tyr
545 550 555 560

Val Asp His Thr Gly Gly Val Asn Gly Thr Lys Ala Leu Tyr Val His
565 570 575

Lys Asp Gly Gly Ile Ser Gln Phe Ile Gly Asp Lys Leu Lys Pro Lys
580 585 590

Thr Glu Tyr Val Ile Gln Tyr Thr Val Lys Gly Lys Pro Ser Ile His
595 600 605

Leu Lys Asp Glu Asn Thr Gly Tyr Ile His Tyr Glu Asp Thr Asn Asn
610 615 620

Asn Leu Glu Asp Tyr Gln Thr Ile Asn Lys Arg Phe Thr Thr Gly Thr
625 630 635 640

Asp Leu Lys Gly Val Tyr Leu Ile Leu Lys Ser Gln Asn Gly Asp Glu
645 650 655

Ala Trp Gly Asp Asn Phe Ile Ile Leu Glu Ile Ser Pro Ser Glu Lys

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660

665

670

Leu Leu Ser Pro Glu Leu Ile Asn Thr Asn Asn Trp Thr Ser Thr Gly
 675 680 685

Ser Thr Asn Ile Ser Gly Asn Thr Leu Thr Leu Tyr Gln Gly Gly Arg
 690 695 700

Gly Ile Leu Lys Gln Asn Leu Gln Leu Asp Ser Phe Ser Thr Tyr Arg
 705 710 715 720

Val Tyr Phe Ser Val Ser Gly Asp Ala Asn Val Arg Ile Arg Asn Ser
 725 730 735

Arg Glu Val Leu Phe Glu Lys Arg Tyr Met Ser Gly Ala Lys Asp Val
 740 745 750

Ser Glu Met Phe Thr Thr Lys Phe Glu Lys Asp Asn Phe Tyr Ile Glu
 755 760 765

Leu Ser Gln Gly Asn Asn Leu Tyr Gly Gly Pro Ile Val His Phe Tyr
 770 775 780

Asp Val Ser Ile Lys
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<210> 6
 <211> 2364
 <212> DNA
 <213> Bacillus thuringiensis

<220>
 <221> misc_feature
 <222> (1)..(2364)
 <223> vip3B native coding sequence.

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 tacctaagta aacaattgca agaaatttcc gacaagttag atgtcattaa cgtgaatgta 480

60163PCT SEQ listing

cttattaact ctacacttac tgaaattaca cctgcgtatc aacggatgaa atatgtaaat	540
gaaaaatttg aagatttaac ttttgctaca gaaaccactt taaaagtaaa aaagaatagc	600
tcccctgcag atattcttga tgagttaact gagttaactg aactagcgaa aagtgtaaaca	660
aaaaatgacg tggatggttt tgaattttac cttaatacat tccacgatgt aatggtagga	720
aacaatttat tcgggcgttc agctttaaaa actgcttcgg aattaatcgc taaagaaaat	780
gtgaaaacaa gtggcagtgga ggtaggaaat gtttataatt tcttaattgt attaacagct	840
ctgcaagcaa aagcttttct tactttaaca acatgccgga aattattagg cttagcagat	900
attgattata ctttcattat gaatgaacat ttagataagg aaaaagagga atttagagta	960
aatatccttc ctacactttc taatactttt tctaactcta actatgcaaa agctaaagga	1020
agcaatgaag atgcaaagat aattgtggaa gctaaaccag gatatgcttt ggttggattt	1080
gaaatgagca atgattcaat cacagtatta aaagcatatc aggctaagct aaaacaagat	1140
tatcaagttg ataaagattc gttatcagaa attgtctatg gtgatatgga taaattattg	1200
tgccccgatac aatctgaaca aatatattat acaaataaca ttgcttttcc caatgaatat	1260
gtaattacta aaattacttt tactaaaaaa atgaatagtt taagatatga ggcaacagct	1320
aatttttatg attcttctac aggggatatt gatctaaata agacaaaagt agaatcaagt	1380
gaagcagagt atagtacgct aagtgctagt actgatggag tctatatgcc gttaggtatt	1440
atcagtgaaa cttttttgac tccaattaat gggtttgga tcgtagtcga tgaaaattca	1500
aaattagtaa atttaacatg taaatcatat ttaagagagg tattattagc aacagactta	1560
agtaataaag aaactaaatt gattgtccca cctattgggt ttattagcaa tattgtagaa	1620
aatgggaact tagagggaga aaacttagag ccgtggaaag caaataacaa aaatgcgtat	1680
gtagatcata caggcggcgt aaatgggaact aaagctttat atgttcataa ggatggtag	1740
ttttcacaat ttattggaga taagttgaaa tcgaaaacag aatatgtaat tcaatatatt	1800
gtaaaggga aagcttctat tcttttgaaa gatgaaaaaa atggtgattg cttttatgaa	1860
gatacaaata atggtttaga agattttcaa accattacta aaagttttat tacaggaacg	1920
gattcttcag gagttcattt aatatttaat agtcaaaatg gcgatgaagc atttggggaa	1980
aactttacta tttcagaaat taggctttcc gaagatttat taagtccaga attgataaat	2040
tcagatgctt gggttggatc tcagggaact tggatctcag gaaattcact cactattaat	2100
agtaatgtga atggaacttt tcgacaaaac ctttcgttag aaagctattc aacttatagt	2160
atgaacttta atgtgaatgg atttgccaag gtgacagtaa gaaattccc tgaagtatta	2220
tttgaaaaaa attatccgca gctttcacct aaagatattt ctgaaaaatt cacaactgca	2280
gccaataata ccgggttgta tgtagagctt tctcgtttta catcgggtgg cgctataaat	2340
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60163PCT SEQ listing

<210> 7
 <211> 787
 <212> PRT
 <213> Bacillus thuringiensis

<220>
 <221> MISC_FEATURE
 <222> (1)..(787)
 <223> Vip3B Toxin

<400> 7

Met Asn Lys Asn Asn Thr Lys Leu Asn Ala Arg Ala Leu Pro Ser Phe
 1 5 10 15

Ile Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile Lys Asp
 20 25 30

Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asn Leu Thr Leu
 35 40 45

Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Glu Ile Ser Gly Lys
 50 55 60

Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly Asn
 65 70 75 80

Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn Glu Gln
 85 90 95

Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu Asn Ala Ile Asn Thr
 100 105 110

Met Leu His Ile Tyr Leu Pro Lys Ile Thr Ser Met Leu Asn Asp Val
 115 120 125

Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Ile Glu Tyr Leu Ser Lys
 130 135 140

Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Val Ile Asn Val Asn Val
 145 150 155 160

Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Met
 165 170 175

Lys Tyr Val Asn Glu Lys Phe Glu Asp Leu Thr Phe Ala Thr Glu Thr
 180 185 190

60163PCT SEQ listing

Thr Leu Lys Val Lys Lys Asn Ser Ser Pro Ala Asp Ile Leu Asp Glu
 195 200 205
 Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val
 210 215 220
 Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val Gly
 225 230 235 240
 Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile
 245 250 255
 Ala Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr
 260 265 270
 Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Lys Ala Phe Leu Thr
 275 280 285
 Leu Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp Tyr Thr
 290 295 300
 Phe Ile Met Asn Glu His Leu Asp Lys Glu Lys Glu Glu Phe Arg Val
 305 310 315 320
 Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala
 325 330 335
 Lys Ala Lys Gly Ser Asn Glu Asp Ala Lys Ile Ile Val Glu Ala Lys
 340 345 350
 Pro Gly Tyr Ala Leu Val Gly Phe Glu Met Ser Asn Asp Ser Ile Thr
 355 360 365
 Val Leu Lys Ala Tyr Gln Ala Lys Leu Lys Gln Asp Tyr Gln Val Asp
 370 375 380
 Lys Asp Ser Leu Ser Glu Ile Val Tyr Gly Asp Met Asp Lys Leu Leu
 385 390 395 400
 Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Asn Asn Ile Ala Phe
 405 410 415
 Pro Asn Glu Tyr Val Ile Thr Lys Ile Thr Phe Thr Lys Lys Met Asn
 420 425 430
 Ser Leu Arg Tyr Glu Ala Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly
 435 440 445

60163PCT SEQ listing

Asp Ile Asp Leu Asn Lys Thr Lys Val Glu Ser Ser Glu Ala Glu Tyr
450 455 460

Ser Thr Leu Ser Ala Ser Thr Asp Gly Val Tyr Met Pro Leu Gly Ile
465 470 475 480

Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Ile Val Val
485 490 495

Asp Glu Asn Ser Lys Leu Val Asn Leu Thr Cys Lys Ser Tyr Leu Arg
500 505 510

Glu Val Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile
515 520 525

Val Pro Pro Ile Gly Phe Ile Ser Asn Ile Val Glu Asn Gly Asn Leu
530 535 540

Glu Gly Glu Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn Ala Tyr
545 550 555 560

Val Asp His Thr Gly Gly Val Asn Gly Thr Lys Ala Leu Tyr Val His
565 570 575

Lys Asp Gly Glu Phe Ser Gln Phe Ile Gly Asp Lys Leu Lys Ser Lys
580 585 590

Thr Glu Tyr Val Ile Gln Tyr Ile Val Lys Gly Lys Ala Ser Ile Leu
595 600 605

Leu Lys Asp Glu Lys Asn Gly Asp Cys Ile Tyr Glu Asp Thr Asn Asn
610 615 620

Gly Leu Glu Asp Phe Gln Thr Ile Thr Lys Ser Phe Ile Thr Gly Thr
625 630 635 640

Asp Ser Ser Gly Val His Leu Ile Phe Asn Ser Gln Asn Gly Asp Glu
645 650 655

Ala Phe Gly Glu Asn Phe Thr Ile Ser Glu Ile Arg Leu Ser Glu Asp
660 665 670

Leu Leu Ser Pro Glu Leu Ile Asn Ser Asp Ala Trp Val Gly Ser Gln
675 680 685

Gly Thr Trp Ile Ser Gly Asn Ser Leu Thr Ile Asn Ser Asn Val Asn
690 695 700

60163PCT SEQ listing

Gly Thr Phe Arg Gln Asn Leu Ser Leu Glu Ser Tyr Ser Thr Tyr Ser
705 710 715 720

Met Asn Phe Asn Val Asn Gly Phe Ala Lys Val Thr Val Arg Asn Ser
725 730 735

Arg Glu Val Leu Phe Glu Lys Asn Tyr Pro Gln Leu Ser Pro Lys Asp
740 745 750

Ile Ser Glu Lys Phe Thr Thr Ala Ala Asn Asn Thr Gly Leu Tyr Val
755 760 765

Glu Leu Ser Arg Phe Thr Ser Gly Gly Ala Ile Asn Phe Arg Asn Phe
770 775 780

Ser Ile Lys
785

<210> 8
<211> 2407
<212> DNA
<213> Bacillus thuringiensis

<220>
<221> misc_feature
<222> (1)..(2406)
<223> vip3Z native coding sequence.

<400> 8
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atztatggat ttgccactgg tatcaaagac attatgaaca tgatttttaa aacggataca 120
gggtggtggtta atttaacact agatgaaatt ttaaagaatc aagatttatt aaatcaaatc 180
tcagataaac tcgatggaat taatggagat ttaggtgatc ttattgcaca aggcaattta 240
aattcagaac taactaagga attattaaaa attgcgaatg agcagaatct gatgttaaatt 300
aatgttaatg ctcaacttaa ttcaataaat tcaacactta acacctatct gccaaaaatt 360
acatctatgc taagtgaggt aatgaaacaa aactatgtat taagtctaca aatagaattt 420
cttagtgaac aattacaaga aatatcagat aaacttgatg ttatcaattt aaatgtatta 480
attaactcta cattgacaga aattacgcct gcatatcaac gtattaaata tgtaaatgat 540
aaatttgatg aattgacttc tactgtggaa aaaaatccga aaattaatca agataatttt 600
actgaagatg ttattgataa ttttaactgat ttaactgaac tagcacgaag tgtaacgaga 660
aatgatatgg atagttttga attttatatt aaaactttcc atgatgtgat gataggaaat 720
aatattattca gtcgttctgc attaaaaact gcttcagaat taattgctaa ggaaaatata 780

60163PCT SEQ listing

catactatgg	gaagtgaaat	tggtaatgtc	tacactttta	tggttgtttt	gacttcctta	840
caagcaaaag	cgttcctaac	tttaactgca	tgccgtaa	tattaggatt	aacagatatac	900
gattatacac	aaattatgaa	tgaaaattta	aatagagaaa	aagaggaatt	tcgcttaa	960
attcttccta	cacttttcta	tgatttttct	aatcctaatt	atacagaaac	tttaggaagt	1020
gatctttag	atcctattgt	tacgttagaa	gctgatcctg	gttatgcttt	aatagggtttt	1080
gagatttcta	atgatccact	tccagtatta	aaagtata	aggcaaagct	aaaaccaa	1140
tatcaagtcg	acaaagagtc	gattatggaa	aatatttatg	gaaatatcca	caaactactt	1200
tgtccaaaac	aacgtcacca	aaaatattat	ataaaagaca	ttacatttcc	tgaaggttat	1260
gtaatcacca	aaattgtttt	tgaaaaaaa	ttgaatctat	taggatatga	agtaacagca	1320
aatctttatg	accattttac	aggaagtatac	gatttgaata	agactattct	agaatcatgg	1380
aaggaagaat	gctgtgaaga	agaatgctgt	gaagaagaat	gctgtgaaga	agaatgctgt	1440
gaagaattat	ataaaattat	agaggcggat	actaacggtg	tttatatgcc	gttgggagta	1500
attagtga	catttttaac	accaatctat	agttttaaac	taattattga	cgaaagaaca	1560
aagagaatat	ctttagcggg	taaatcttat	ttacgtgaat	ctttactagc	cacagattta	1620
gttaataaag	atacgaattt	aattccttca	cccaatgggt	tcattaacag	tattgtggaa	1680
aattggaata	taacatcgga	taatatagag	ccctggaaag	cgaataataa	aatgcatat	1740
gtcgataaga	cggatgacat	ggtgggattt	aactctttat	atactcataa	ggatggggaa	1800
ttcttgcaat	ttattggagc	taagttaaag	gctaaaactg	agtatatcat	tcaatatact	1860
gtaaaagggg	gtccggaagt	ttatttgaaa	aacaataaag	gtatctttta	tgaggataca	1920
acaaataaat	ttgatacggt	tcaaaactata	actaaaaagt	tcaattcagg	agtagatcca	1980
tccgaaatat	atctagtttt	taaaaatcaa	attggatatg	aagcatgggg	aaataaattt	2040
attatactag	aatcaagtc	atttgaaacc	ctaccacaaa	tattaaaacc	tgaaaattgg	2100
atgccttttg	gtaatgctga	gattaaagaa	gatggaaaaa	ttgagatttc	aggtaatgga	2160
actatgacgc	aaaatattca	attagaacag	aattccaagt	atcatctaag	atcttctgta	2220
aaaggaaaag	ggagagtagc	gatacaaact	caaagctccc	atataaatgt	accagctaca	2280
aacgaagagg	tttctacaat	gattacaact	agaaacttat	acggtgaagg	tatgatatac	2340
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gaatagg						2407

<210> 9
 <211> 801
 <212> PRT
 <213> *Bacillus thuringiensis*

60163PCT SEQ listing

<220>

<221> MISC_FEATURE

<222> (1)..(801)

<223> Vip3Z toxin

<400> 9

Met Asn Asn Thr Lys Leu Asn Ala Arg Ala Leu Pro Ser Phe Ile Asp
1 5 10 15

Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile Lys Asp Ile Met
20 25 30

Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Gly Asn Leu Thr Leu Asp
35 40 45

Glu Ile Leu Lys Asn Gln Asp Leu Leu Asn Gln Ile Ser Asp Lys Leu
50 55 60

Asp Gly Ile Asn Gly Asp Leu Gly Asp Leu Ile Ala Gln Gly Asn Leu
65 70 75 80

Asn Ser Glu Leu Thr Lys Glu Leu Leu Lys Ile Ala Asn Glu Gln Asn
85 90 95

Leu Met Leu Asn Asn Val Asn Ala Gln Leu Asn Ser Ile Asn Ser Thr
100 105 110

Leu Asn Thr Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser Glu Val Met
115 120 125

Lys Gln Asn Tyr Val Leu Ser Leu Gln Ile Glu Phe Leu Ser Glu Gln
130 135 140

Leu Gln Glu Ile Ser Asp Lys Leu Asp Val Ile Asn Leu Asn Val Leu
145 150 155 160

Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile Lys
165 170 175

Tyr Val Asn Asp Lys Phe Asp Glu Leu Thr Ser Thr Val Glu Lys Asn
180 185 190

Pro Lys Ile Asn Gln Asp Asn Phe Thr Glu Asp Val Ile Asp Asn Leu
195 200 205

Thr Asp Leu Thr Glu Leu Ala Arg Ser Val Thr Arg Asn Asp Met Asp
210 215 220

60163PCT SEQ listing

Ser Phe Glu Phe Tyr Ile Lys Thr Phe His Asp Val Met Ile Gly Asn
 225 230 235 240
 Asn Leu Phe Ser Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile Ala
 245 250 255
 Lys Glu Asn Ile His Thr Met Gly Ser Glu Ile Gly Asn Val Tyr Thr
 260 265 270
 Phe Met Val Val Leu Thr Ser Leu Gln Ala Lys Ala Phe Leu Thr Leu
 275 280 285
 Thr Ala Cys Arg Lys Leu Leu Gly Leu Thr Asp Ile Asp Tyr Thr Gln
 290 295 300
 Ile Met Asn Glu Asn Leu Asn Arg Glu Lys Glu Glu Phe Arg Leu Asn
 305 310 315 320
 Ile Leu Pro Thr Leu Ser Asn Asp Phe Ser Asn Pro Asn Tyr Thr Glu
 325 330 335
 Thr Leu Gly Ser Asp Leu Val Asp Pro Ile Val Thr Leu Glu Ala Asp
 340 345 350
 Pro Gly Tyr Ala Leu Ile Gly Phe Glu Ile Leu Asn Asp Pro Leu Pro
 355 360 365
 Val Leu Lys Val Tyr Gln Ala Lys Leu Lys Pro Asn Tyr Gln Val Asp
 370 375 380
 Lys Glu Ser Ile Met Glu Asn Ile Tyr Gly Asn Ile His Lys Leu Leu
 385 390 395 400
 Cys Pro Lys Gln Arg His Gln Lys Tyr Tyr Ile Lys Asp Ile Thr Phe
 405 410 415
 Pro Glu Gly Tyr Val Ile Thr Lys Ile Val Phe Glu Lys Lys Leu Asn
 420 425 430
 Leu Leu Gly Tyr Glu Val Thr Ala Asn Leu Tyr Asp Pro Phe Thr Gly
 435 440 445
 Ser Ile Asp Leu Asn Lys Thr Ile Leu Glu Ser Trp Lys Glu Glu Cys
 450 455 460
 Cys Glu Glu Glu Cys Cys Glu Glu Glu Cys Cys Glu Glu Glu Cys Cys
 465 470 475 480

60163PCT SEQ listing

Glu Glu Leu Tyr Lys Ile Ile Glu Ala Asp Thr Asn Gly Val Tyr Met
485 490 495

Pro Leu Gly Val Ile Ser Glu Thr Phe Leu Thr Pro Ile Tyr Ser Phe
500 505 510

Lys Leu Ile Ile Asp Glu Arg Thr Lys Arg Ile Ser Leu Ala Gly Lys
515 520 525

Ser Tyr Leu Arg Glu Ser Leu Leu Ala Thr Asp Leu Val Asn Lys Asp
530 535 540

Thr Asn Leu Ile Pro Ser Pro Asn Gly Phe Ile Asn Ser Ile Val Glu
545 550 555 560

Asn Trp Asn Ile Thr Ser Asp Asn Ile Glu Pro Trp Lys Ala Asn Asn
565 570 575

Lys Asn Ala Tyr Val Asp Lys Thr Asp Asp Met Val Gly Phe Asn Ser
580 585 590

Leu Tyr Thr His Lys Asp Gly Glu Phe Leu Gln Phe Ile Gly Ala Lys
595 600 605

Leu Lys Ala Lys Thr Glu Tyr Ile Ile Gln Tyr Thr Val Lys Gly Ser
610 615 620

Pro Glu Val Tyr Leu Lys Asn Asn Lys Gly Ile Phe Tyr Glu Asp Thr
625 630 635 640

Thr Asn Lys Phe Asp Thr Phe Gln Thr Ile Thr Lys Lys Phe Asn Ser
645 650 655

Gly Val Asp Pro Ser Glu Ile Tyr Leu Val Phe Lys Asn Gln Ile Gly
660 665 670

Tyr Glu Ala Trp Gly Asn Lys Phe Ile Ile Leu Glu Ile Lys Ser Phe
675 680 685

Glu Thr Leu Pro Gln Ile Leu Lys Pro Glu Asn Trp Met Pro Phe Gly
690 695 700

Asn Ala Glu Ile Lys Glu Asp Gly Lys Ile Glu Ile Ser Gly Asn Gly
705 710 715 720

Thr Met Thr Gln Asn Ile Gln Leu Glu Gln Asn Ser Lys Tyr His Leu

60163PCT SEQ listing

725

730

735

Arg Phe Ser Val Lys Gly Lys Gly Arg Val Ala Ile Gln Thr Gln Ser
740 745 750

Ser His Ile Asn Val Pro Ala Thr Asn Glu Glu Val Ser Thr Met Ile
755 760 765

Thr Thr Arg Asn Leu Tyr Gly Glu Gly Met Ile Tyr Leu Phe Asn Asp
770 775 780

Asp Val Glu Asn Ser Lys Val Ile Phe Ser Asp Val Ser Leu Val Lys
785 790 795 800

Glu

<210> 10
<211> 2367
<212> DNA
<213> Artificial Sequence

<220>
<223> vip3A-C Hybrid toxin coding sequence.

<400> 10
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aatggcattt atggatttgc cactggtatc aaagacatta tgaacatgat ttttaaaacg 120
gatacaggtg gtgatctaac cctagacgaa attttaaaga atcagcagtt actaaatgat 180
atcttctggta aattggatgg ggtgaatgga agcttaaagt atcttatcgc acagggaaac 240
ttaaatacag aattatctaa ggaaatatta aaaattgcaa atgaacaaaa tcaagtttta 300
aatgatgtta ataacaaact cgatgcgata aatacgatgc ttcgggtata tctacctaaa 360
attacctcta tgttgagtga tgtaatgaaa caaaattatg cgctaagtct gcaaatagaa 420
tacttaagta aacaattgca agagatttct gataagttgg atattattaa tgtaaagtga 480
cttattaact ctacacttac tgaaattaca cctgcgtatc aaaggattaa atatgtgaac 540
gaaaaatttg aggaattaac ttttgctaca gaaactagtt caaaagtaaa aaaggatggc 600
tctcctgcag atattcttga tgagttaact gagttaactg aactagcgaa aagtgttaaca 660
aaaaatgatg tggatggttt tgaattttac ctttaatacat tccacgatgt aatggtagga 720
aataatttat tcgggcgttc agctttaaaa actgcatcgg aattaattac taaagaaaat 780
gtgaaaacaa gtggcagtga ggtcggaaat gtttataact tcttaattgt attaacagct 840
ctgcaagcaa aagcttttct tactttaaca acatgccgaa aattattagg cttagcagat 900
attgattata cttctattat gaatgaacat ttaaataagg aaaaagagga atttagagta 960

60163PCT SEQ listing

aacatcctcc ctacactttc taatactttt tctaataccta attatgcaaa agttaaaagga	1020
agtgatgaag atgcaaagat gattgtggaa gctaaaccag gacatgcatt gattgggttt	1080
gaaattagta atgattcaat tacagtatta aaagtatatg aggctaagct aaaacaaaat	1140
tatcaagtcg ataaggattc cttatcggaa gttattttatg gtgatatgga taaattattg	1200
tgcccagatc aatctgaaca aatctattat acaataaca tagtatttcc aaatgaatat	1260
gtaattacta aaattgattt cactaaaaaa atgaaaactt taagatatga ggtaacagcg	1320
aatTTTTatg attcttctac aggagaaatt gacttaaata agaaaaaagt agaatcaagt	1380
gaagcggagt atagaacgtt aagtgcctaat gatgatgggg tgtatatgcc gttagggtgc	1440
atcagtgaat catttttgac tccgattaat gggtttggcc tccaagctga tgaaaattca	1500
agattaatta ctttaacatg taaatcatat ttaagagaac tactgctagc aacagactta	1560
agcaataaag aaactaaatt gatcgtcccg ccaagtgggt ttattagcaa tattgtagag	1620
aacgggtcca tagaagagga caatttagag ccgtggaaag caaataataa gaatgcgtat	1680
gtagatcata caggcggagt gaatggaact aaagctttat atgttcataa ggacggagga	1740
atttcacaat ttattggaga taagttaaaa ccgaaaactg agtatgtaat ccaatatact	1800
gttaaaggaa aaccttctat tcatttaaaa gatgaaaata ctggatatat tcattatgaa	1860
gatacaaata ataatttaga agattatcaa actattaata aacgttttac tacaggaact	1920
gatttaaagg gagtgtattt aattttaaaa agtcaaaatg gagatgaagc ttggggagat	1980
aaatttaca ttttagaaat taagcctgag gaggatttat taagcccaga attaattaat	2040
ccgaattctt ggattacgac tccaggggct agcatttcag gaaataaact tttcattaac	2100
ttggggacaa atgggacctt tagacaaagt ctttcattaa acagttattc aacttatagt	2160
ataagcttta ctgcatcagg accatttaat gtgacggtaa gaaattctag gggagtatta	2220
tttgaacgaa gcaaccttat gtcttcaact agtcatattt ctgggacatt caaaactgaa	2280
tccaataata ccggattata tgtagaactt tcccgtcgct ctggtggtgg tggatcatata	2340
tcatttgaaa acgtttctat taaataa	2367

<210> 11
 <211> 788
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Hybrid Vip3A-C toxin

<400> 11

Met	Asn	Lys	Asn	Asn	Thr	Lys	Leu	Ser	Thr	Arg	Ala	Leu	Pro	Ser	Phe
1			5						10					15	

60163PCT SEQ listing

Ile Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile Lys Asp
 20 25 30
 Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asp Leu Thr Leu
 35 40 45
 Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Asp Ile Ser Gly Lys
 50 55 60
 Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly Asn
 65 70 75 80
 Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn Glu Gln
 85 90 95
 Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu Asp Ala Ile Asn Thr
 100 105 110
 Met Leu Arg Val Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser Asp Val
 115 120 125
 Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Ile Glu Tyr Leu Ser Lys
 130 135 140
 Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile Ile Asn Val Asn Val
 145 150 155 160
 Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile
 165 170 175
 Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr Glu Thr
 180 185 190
 Ser Ser Lys Val Lys Lys Asp Gly Ser Pro Ala Asp Ile Leu Asp Glu
 195 200 205
 Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val
 210 215 220
 Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val Gly
 225 230 235 240
 Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile
 245 250 255
 Thr Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr
 260 265 270

60163PCT SEQ listing

Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Lys Ala Phe Leu Thr
 275 280 285
 Leu Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp Tyr Thr
 290 295 300
 Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg Val
 305 310 315 320
 Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala
 325 330 335
 Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu Ala Lys
 340 345 350
 Pro Gly His Ala Leu Ile Gly Phe Glu Ile Ser Asn Asp Ser Ile Thr
 355 360 365
 Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln Val Asp
 370 375 380
 Lys Asp Ser Leu Ser Glu Val Ile Tyr Gly Asp Met Asp Lys Leu Leu
 385 390 395 400
 Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Asn Asn Ile Val Phe
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60163PCT SEQ listing

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60163PCT SEQ listing

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60163PCT SEQ listing

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Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asn Leu Thr Leu
35 40 45

Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Glu Ile Ser Gly Lys
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Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly Asn
Page 39

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75

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60163PCT SEQ listing

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60163PCT SEQ listing

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60163PCT SEQ listing

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60163PCT SEQ listing

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